

IN THE CLAIM

No claim has been amended.

1 1. (Original) A method for determining gender from a human DNA sample, said method
2 comprising:

3 providing a human DNA sample, said DNA sample containing X chromosomal material
4 and potentially containing Y chromosomal material;

5 selecting at least one locus from a non-combining X-Y homologous region, said region
6 containing a monomorphic *Alu* insertion in one of the X chromosome and the Y chromosome;

7 amplifying the selected locus of the DNA sample in an amplification reaction, wherein
8 the product of the reaction is a mixture of amplified alleles from the amplified locus present in
9 the sample; and

10 determining the gender of the DNA sample by evaluating the amplified alleles in terms of
11 size and number.

1 2. (Original) The method of claim 1, wherein said amplification reaction is a polymerase
2 chain reaction.

1 3. (Original) The process of claim 2, wherein the amplification step comprises an
2 amplification of an *AluSTY α* locus.

1 4. (Original) The method of claim 3, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4 and

5 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 5. (Original) The process of claim 2, wherein the amplification step comprises an
2 amplification of an *AluSTXa* locus.

1 6. (Original) The method of claim 5, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

4 and

5 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 7. (Original) The process of claim 2, wherein said amplification step comprises an
2 amplification of an *AluSTXa* locus and an amplification of an *AluSTYa*.

1 8. (Original) The method of claim 7, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 for said amplification of the *AluSTXa* locus, 5'- TGAAGAAATTCAGTTCATAGCTTGT
4 -3' (SEQ ID NO: 3) and 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and
5 for said amplification of the *AluSTYa*, 5'- CATGTATTTGATGGGGATAGAGG -3'
6 (SEQ ID NO: 1) and 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 9. (Original) The method of claim 2, wherein at least one primer of each pair has a
2 fluorescent label covalently attached thereto.

1 10. (Original) The method of claim 1, wherein the sizes of the amplified alleles are
2 evaluated by fragment resolution on an agarose gel.

1 11. (Original) The method of claim 10, wherein the sizes of the amplified alleles are
2 evaluated by comparison with a size standard such that:

3 for a Y insertion *AluSTYa* an *Alu* filled site for Y chromosome has size approximately
4 528 base pairs and an empty site for X chromosome has size approximately 199 base pairs; or

5 for an X insertion *AluSTXa* an *Alu* filled site for X chromosome has size approximately
6 878 base pairs and an empty site for Y chromosome has size approximately 556 base pairs.

1 12. (Original) The method of claim 1, wherein male gender is characterized by presence
2 of two DNA fragments and female gender is characterized by presence of one DNA fragment,
3 for amplified loci.

1 13. (Original) A primer pair adapted for assaying a Y insertion in a sex determination of
2 human cells, each primer pair having the sequence selected from, or constituting a subset of, the
3 group consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 14. (Original) A primer pair adapted for assaying an X insertion in a sex determination
2 of human cells, each primer having the sequence selected from, or constituting a subset of, the
3 group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 15. (Original) A kit adapted for analyzing alleles of an *AluSTYa* locus on an Y
2 chromosome, said kit comprising a primer pair, each primer of the primer pair having the
3 sequence selected from, or constituting a subset of, the group consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 16. (Original) A kit adapted for analyzing alleles of an *AluSTXa* locus on a X
2 chromosome, said kit comprising a primer pair wherein each primer of the primer pair has the
3 sequence selected from, or constituting a subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 17. (Original) A kit for determining gender from a sample, comprising:
2 polymerase chain reaction reagents comprising a polymerase and buffer; and
3 a pair of primers to amplify at least one locus in a non-combining X-Y homologous
4 region of the DNA sample, said locus containing a monomorphic *Alu* insertion.

1 18. (Original) The kit of claim 17, wherein said locus is an *AluSTYa* locus.

1 19. (Original) The kit of claim 18, wherein said primer pairs containing the following
2 sequences:

3 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4 and

5 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 20. (Original) The kit of claim 17, wherein said locus is an *AluSTXa* locus.

1 21. (Original) The kit of claim 20, wherein said primer pairs containing the following
2 sequences:

3 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

4 and

5 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 22. (Original) The kit of claim 17, wherein said at least one locus comprises an *AluSTY_a*
2 locus and an *AluSTX_a* locus.

1 23. (Original) The kit of claim 22, wherein said pair of primers comprises:
2 a first primer pair, wherein each primer of the first primer pair has the sequence selected
3 from, or constituting a subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and

7 a second primer pair, wherein each primer of the second primer pair has the sequence
8 selected from, or constituting a subset of, the group consisting of:

9 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

10 and

Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

24. (Original) A method for quantitating male DNA in a sample, said method comprising the steps of:

amplifying a locus in the sample by a polymerase chain reaction, wherein said locus is in a non-combining X-Y homologous region and contains a monomorphic *Alu* insertion;

detecting the product of the amplified locus; and

comparing the detected result with a result of standard male DNA to quantitate DNA in a sample.

25. (Original) The method of claim 24, wherein the locus is *AluSTYa*, *AluSTXa*, or both *AluSTYa* and *AluSTXa*.

26. (Original) The method of claim 25, wherein said amplification step comprises the step of using primer pairs containing at least one of the following pair of sequences:

5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3) and

5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and

5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1) and

5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).